

Re-run

#11



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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,701A

DATE: 08/18/2004

TIME: 12:33:20

Input Set : N:\DA\US09931701A.raw

Output Set: N:\CRF4\08102004\I931701A.raw

1 <110> APPLICANT: Outtrup, Helle
 2 Pedersen, Poul
 3 Sorensen, Marianne
 4 <120> TITLE OF INVENTION: Subtilase Enzymes
 5 <130> FILE REFERENCE: 10065.200-US
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/931,701A
 7 <141> CURRENT FILING DATE: 2001-08-16
 8 <160> NUMBER OF SEQ ID NOS: 9
 9 <170> SOFTWARE: PatentIn version 3.1
 11 <210> SEQ ID NO: 1
 12 <211> LENGTH: 1143
 13 <212> TYPE: DNA
 14 <213> ORGANISM: Bacillus clausii
 15 <220> FEATURE:
 16 <221> NAME/KEY: CDS
 17 <222> LOCATION: (1)..(1140)
 18 <223> OTHER INFORMATION:
 19 <221> NAME/KEY: mat_peptide
 20 <222> LOCATION: (334)..()
 21 <223> OTHER INFORMATION:

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 24 Met Asn Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
 25 -110 -105 -100
 26 att tct gtc gct ttt agt tca tcg att gca tcg gct gct gaa gaa gca 93
 27 Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala
 28 -95 -90 -85
 29 aaa gaa aaa tac tta att ggc ttt aat gaa cag gaa gct gtc agt gag 141
 30 Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu
 31 -80 -75 -70 -65
 32 ttt gtc gaa caa gta gat gca aat aat gat gtc gcc gtt ctc tct gag 189
 33 Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu
 34 -60 -55 -50
 35 gaa gag gaa gtc gaa att gaa ctg ctt cat gag ttc gaa acc att ccc 237
 36 Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro
 37 -45 -40 -35
 38 gtt tta tca gta gag tta agc cca gaa gat gtg gat acg ctt gaa ctc 285
 39 Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu
 40 -30 -25 -20
 41 gat cca gcg att tct tac att gag gaa gat gta gaa gta tcg att atg 333
 42 Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met
 43 -15 -10 -5 -1
 44 gct cag tct gtg cca tgg gga att agc cgt gtg caa gca cct gcc gcc 381

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45	Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala	
46	1 5 10 15	
47	cat aac cgc gga gtg aca ggt tcc ggt gta aaa gtt gct gtt ctt gat	429
48	His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp	
49	20 25 30	
50	aca ggc att tcc gcc cat cca gac tta aat atc cgc ggc ggt gct agc	477
51	Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser	
52	35 40 45	
53	ttt gtg aca ggc gag cca acg tat caa gat ggc aat gga cac ggc acg	525
54	Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr	
55	50 55 60	
56	cat gtg gca ggg acg att gcc gct tta aac aat tcg att ggc gtc ctt	573
57	His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu	
58	65 70 75 80	
59	ggc gta gcg cct aat gct gaa cta tac gct gtt aaa gta tta gca gcc	621
60	Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala	
61	85 90 95	
62	aac ggc aga ggc cca gtc agc tca att gcc caa ggg ttg gaa tgg gca	669
63	Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala	
64	100 105 110	
65	gga aac aat ggc atg gac gtt gcc aac ttg agt tta gga agt cca tcg	717
66	Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser	
67	115 120 125	
68	cca agc gca acg ctt gag caa gcg gtt aat agc gct act tct aga ggc	765
69	Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly	
70	130 135 140	
71	gtc ctt gtc gta gca gca act gga aac tca gga aca ggc tcc ctc gac	813
72	Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp	
73	145 150 155 160	
74	tac cca gct cgt tat gcg aac gct atg gca gtc gga gct act gac caa	861
75	Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln	
76	165 170 175	
77	aac aac aac cgc gcc agc ttt tct cag tac gga gca ggg ctt gac att	909
78	Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile	
79	180 185 190	
80	gtt gcg cca ggt gta aac gtg cag agc aca tac cca ggt tca act tac	957
81	Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr	
82	195 200 205	
83	195 200 205	
84	gct agc ttc aac ggt aca tcg atg gcg act cct cac gtt gtc ggt gta	1005
85	Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val	
86	210 215 220	
87	gca gcc ctt gta aaa caa aaa aac cca tct tgg tcc aat gta caa atc	1053
88	Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile	
89	225 230 235 240	
90	cgc aat cat cta aag aat aca gcc aca agt ttg ggt agc acg aac ttg	1101
91	Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu	
92	245 250 255	
93	tat gga agc ggg ctt gtc aat gca gaa gca gca aca cgc taa	1143
	Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Thr Arg	

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Input Set : N:\DA\US09931701A.raw
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94	260	265
96 <210>	SEQ ID NO: 2	
97 <211>	LENGTH: 380	
98 <212>	TYPE: PRT	
99 <213>	ORGANISM: Bacillus clausii	
100 <400>	SEQUENCE: 2	
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102 -110	-105	-100
103 Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala		
104 -95	-90	-85
105 Lys Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu		
106 -80	-75	-70
107 Phe Val Glu Gln Val Asp Ala Asn Asn Asp Val Ala Val Leu Ser Glu		
108 -60	-55	-50
109 Glu Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro		
110 -45	-40	-35
111 Val Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Thr Leu Glu Leu		
112 -30	-25	-20
113 Asp Pro Ala Ile Ser Tyr Ile Glu Glu Asp Val Glu Val Ser Ile Met		
114 -15	-10	-5
115 Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala		
116 1 5 10 15		
117 His Asn Arg Gly Val Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp		
118 20 25 30		
119 Thr Gly Ile Ser Ala His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser		
120 35 40 45		
121 Phe Val Thr Gly Glu Pro Thr Tyr Gln Asp Gly Asn Gly His Gly Thr		
122 50 55 60		
123 His Val Ala Gly Thr Ile Ala Ala Leu Asn Ser Ile Gly Val Leu		
124 65 70 75 80		
125 Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Ala Ala		
126 85 90 95		
127 Asn Gly Arg Gly Pro Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala		
128 100 105 110		
129 Gly Asn Asn Gly Met Asp Val Ala Asn Leu Ser Leu Gly Ser Pro Ser		
130 115 120 125		
131 Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly		
132 130 135 140		
133 Val Leu Val Val Ala Ala Thr Gly Asn Ser Gly Thr Gly Ser Leu Asp		
134 145 150 155 160		
135 Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln		
136 165 170 175		
137 Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile		
138 180 185 190		
139 Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr		
140 195 200 205		
141 Ala Ser Phe Asn Gly Thr Ser Met Ala Thr Pro His Val Val Gly Val		
142 210 215 220		
143 Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile		

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Input Set : N:\DA\US09931701A.raw
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144	225	230	235	240
145	Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu			
146	245	250		255
147	Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg			
148	260	265		
150	<210> SEQ ID NO: 3			
151	<211> LENGTH: 5			
152	<212> TYPE: PRT			
153	<213> ORGANISM: Artificial Sequence			
154	<220> FEATURE:			
155	<223> OTHER INFORMATION: Synthetic			
156	<400> SEQUENCE: 3			
157	Ala Gly Lys Ala Leu			
158	1	5		
160	<210> SEQ ID NO: 4			
161	<211> LENGTH: 4			
162	<212> TYPE: PRT			
163	<213> ORGANISM: Artificial Sequence			
164	<220> FEATURE:			
165	<223> OTHER INFORMATION: Synthetic			
166	<400> SEQUENCE: 4			
167	Ala Gly Gly Leu			
168	1			
170	<210> SEQ ID NO: 5			
171	<211> LENGTH: 29			
172	<212> TYPE: DNA			
173	<213> ORGANISM: Artificial Sequence			
174	<220> FEATURE:			
175	<223> OTHER INFORMATION: Primer			
176	<400> SEQUENCE: 5			
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179	<210> SEQ ID NO: 6			
180	<211> LENGTH: 32			
181	<212> TYPE: DNA			
182	<213> ORGANISM: Artificial Sequence			
183	<220> FEATURE:			
184	<223> OTHER INFORMATION: Primer			
185	<400> SEQUENCE: 6			
186	tttggatcca tacacaaaaaa aacgctgtgc cc			32
188	<210> SEQ ID NO: 7			
189	<211> LENGTH: 29			
190	<212> TYPE: DNA			
191	<213> ORGANISM: Artificial Sequence			
192	<220> FEATURE:			
193	<223> OTHER INFORMATION: Primer			
194	<400> SEQUENCE: 7			
195	aatagagctc accagcttgg acaagttgg			29
197	<210> SEQ ID NO: 8			
198	<211> LENGTH: 32			

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Input Set : N:\DA\US09931701A.raw
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199 <212> TYPE: DNA
 200 <213> ORGANISM: Artificial Sequence
 201 <220> FEATURE:
 202 <223> OTHER INFORMATION: Primer
 203 <400> SEQUENCE: 8
 204 tttggatcca tacacaaaaa aacgctgtgc cc 32
 206 <210> SEQ ID NO: 9
 207 <211> LENGTH: 275
 208 <212> TYPE: PRT
 209 <213> ORGANISM: Bacillus
 210 <400> SEQUENCE: 9
 211 Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
 212 1 5 10 15
 213 His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
 214 20 25 30
 215 Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
 216 35 40 45
 217 Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
 218 50 55 60
 219 Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
 220 65 70 75 80
 221 Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
 222 85 90 95
 223 Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
 224 100 105 110
 225 Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
 226 115 120 125
 227 Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
 228 130 135 140
 229 Ser Gly Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
 230 145 150 155 160
 231 Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
 232 165 170 175
 233 Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
 234 180 185 190
 235 Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
 236 195 200 205
 237 Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
 238 210 215 220
 239 Pro His Val Ala Gly Ala Ala Leu Ile Leu Ser Lys His Pro Asn
 240 225 230 235 240
 241 Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Lys
 242 245 250 255
 243 Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
 244 260 265 270
 245 Ala Ala Gln
 246 275

VERIFICATION SUMMARY DATE: 08/18/2004
PATENT APPLICATION: US/09/931,701A TIME: 12:33:21

Input Set : N:\DA\US09931701A.raw
Output Set: N:\CRF4\08102004\I931701A.raw

L:6 M:270 C: Current Application Number differs, Wrong Format
L:22 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0